

1st Amino Acid Sequence

: PQQ-dependent glucose dehydrogenase obtained from File Name

Acinetobacter baumannii NCIMB 11517

Sequence Size : 456

2nd Amino Acid Sequence

: PQQ-dependent glucose dehydrogenase obtained from File Name

Acinetobacter calcoaceticus LMD79.417

Sequence Size : 455

Unit Size to Compare = 2 Pick up Location = 1

INT/OPT.Score : < 1346/ 2123 > [93.4% / 455 aa]

1' DIPLTPAQFAKAKTENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKILRVNPVSGSA * **** **** **** **** **** ***

1" DVPLTPSQFAKAKSENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKILRVNPESGSV

61' KTVFOVPEIVSDADGONGLLGFAFHPDFKHNPYIYISGTFKNPKSTDKELPNQTIIRRYT *******

61" KTVFQVPEIVNDADGQNGLLGFAFHPDFKNNPYIYISGTFKNPKSTDKELPNQTIIRRYT

121' YNKTTDTFEKPIDLIAGLPSSKDHQSGRLVIGPDQKIYYTIGDQGRNQLAYLFLPNQAQH ***,***,***,*********

121" YNKSTDTLEKPVDLLAGLPSSKDHQSGRLVIGPDQKIYYTIGDQGRNQLAYLFLPNQAQH

181' TPTOOELNSKDYHTYMGKVLRLNLDGSVPKDNPSFNGVVSHIYTLGHRNPQGLAFAPNGK **********

181" TPTQQELNGKDYHTYMGKVLRLNLDGSIPKDNPSFNGVVSHIYTLGHRNPQGLAFTPNGK

241' LLQSEQGPNSDDEINLVLKGGNYGWPNVAGYKDDSGYAYANYSAATNKSQIKDLAQNGIK **********************

241" LLOSEQGPNSDDEINLIVKGGNYGWPNVAGYKDDSGYAYANYSAAANKS-IKDLAQNGVK

301' VATGVPVTKESEWTGKNFVPPLKTLYTVQDTYNYNDPTCGEMAYICWPTVAPSSAYVYTG *.*********************

300" VAAGVPVTKESEWTGKNFVPPLKTLYTVQDTYNYNDPTCGEMTYICWPTVAPSSAYVYKG TECH CENTER 1600/2900

361' GKKAIPGWENTLLVPSLKRGVIFRIKLDPTYSTTLDDAIPMFKSNNRYRDVIASPEGNTL

360" GKKAITGWENTLLVPSLKRGVIFRIKLDPTYSTTYDDAVPMFKSNNRYRDVIASPDGNVL

421' YVLTDTAGNVQKDDGSVTHTLENPGSLIKFTYNGK *********

420" YVLTDTAGNVQKDDGSVTNTLENPGSLIKFTYKAK

RECEIVED

AUG 2 7 2003